SEQUENCE LISTING

<110> Gurney, et al

<120> ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREOF

<130> 28341/6280NCP

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<141> 2000-09-22

<150> US 60/169,232
<151> 1999-12-06

<150> US 09/416,901
<151> 1999-10-13

<150> US 60/155,493
<151> 1999-09-23

<150> US 09/404,133
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    50   55   60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65   70   75   80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
                85   90   95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
            100   105   110

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Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
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Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
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Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
            180   185   190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
    195   200   205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
    210   215   220

Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
225   230   235   240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
            245   250   255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
    260   265   270

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Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
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Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
            340             345             350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
        355             360             365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
370             375             380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385             390             395             400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
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Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
            420             425             430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
        435             440             445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
    450             455             460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465             470             475             480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg Cys
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Val Arg His Arg Trp Lys
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Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
        35                  40                  45


Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
    50                  55                  60


Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65                  70                  75                  80


Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
                85                  90                  95


Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
                100                 105                 110


Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115                 120                 125


Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
        130                 135                 140


Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
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Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
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Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
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Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210   215   220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225   230   235   240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
              245   250   255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
              260   265   270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
        275   280   285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
        290   295   300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305   310   315   320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
              325   330   335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
              340   345   350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
        355   360   365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
        370   375   380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385   390   395   400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
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Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
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Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
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Ile Ser Leu Leu Lys
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Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
            35   40   45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
        50   55   60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65   70   75   80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
                85   90   95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
                100   105   110

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Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115   120   125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
        130   135   140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145   150   155   160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
                165   170   175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
            180   185   190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
            195   200   205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
        210   215   220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
225   230   235   240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
                245   250   255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
            260   265   270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
            275   280   285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
        290   295   300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
305   310   315   320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
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Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
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Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
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Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
                405             410                 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
                420             425             430

Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
            435             440             445

Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
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ccttaggcac  cacaaacttg  agttggaaat  tttgctgctt  gaagcttcag  ccctgaccct    1800

ctgcccagca  tcctttagag  tctccaacct  aaagtattct  ttatgtcctt  ccagaagtac    1860

tggcgtcata  ctcaggctac  ccggcatgtg  tccctgtggt  accctggcag  agaaagggcc    1920

aatctcattc  cctgctggcc  aaagtcagca  gaagaaggtg  aagtttgcca  gttgctttag    1980

tgatagggac  tgcagactca  agcctacact  ggtacaaaga  ctgcgtcttg  agataaacaa    2040

gaa                                                                      2043


<210>   8
<211>   501
<212>   PRT
<213>   Mus musculus

<400>   8

Met Ala Pro Ala Leu His Trp Leu Leu Leu Trp Val Gly Ser Gly Met
1               5                   10                  15


Leu Pro Ala Gln Gly Thr His Leu Gly Ile Arg Leu Pro Leu Arg Ser
                20                  25                  30


Gly Leu Ala Gly Pro Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
            35                  40                  45


Glu Glu Ser Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
        50                  55                  60
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Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65   70   75   80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
            85   90   95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
        100   105   110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115   120   125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
    130   135   140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145   150   155   160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
            165   170   175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
        180   185   190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro
        195   200   205

Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
    210   215   220

Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225   230   235   240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
            245   250   255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
        260   265   270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
        275   280   285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
    290   295   300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305   310   315   320

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Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
                325                 330                 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
                340                 345                 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
                355                 360                 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
        370                 375                 380

Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385                 390                 395                 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
                405                 410                 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
                420                 425                 430

Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
        435                 440                 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
        450                 455                 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465                 470                 475                 480

Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp
                485                 490                 495

Ile Ser Leu Leu Lys
                500


<210>   9
<211>   2088
<212>   DNA
<213>   Homo sapiens

<400>   9
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cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga     120

ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa     180

acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg     240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg     300
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-14-

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ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt    360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg    420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag    480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga    540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat    600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg    660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa    720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa    780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca    840

gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt    900

gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa    960

gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag   1020

gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc   1080

caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag   1140

acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaac   1200

tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag   1260

aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg   1320

cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt   1380

gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc   1440

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tctttgaccg aaacgaaaac caccgtggag ctccttcccg tgaatggaga gttcagcctg   1620

gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac   1680

gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt   1740

tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc   1800

cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg   1860

ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgtcat agcgacagtg   1920

atcgtcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg   1980

gtggaggttg acgccgctgt cacccccagag gagcgccacc tgtccaagat gcagcagaac   2040

ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag              2088
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<210> 10
<211> 695
<212> PRT
<213> Homo sapiens

<400> 10

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1   5   10   15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
                20   25   30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
                35   40   45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50   55   60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65   70   75   80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85   90   95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
                100   105   110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
                115   120   125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
        130   135   140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145   150   155   160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165   170   175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
                180   185   190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
                195   200   205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
        210   215   220

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Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225             230             235             240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
            245             250             255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
            260             265             270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
        275             280             285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
    290             295             300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305             310             315             320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
            325             330             335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
            340             345             350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
        355             360             365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
    370             375             380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385             390             395             400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
            405             410             415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
            420             425             430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
        435             440             445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
    450             455             460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465             470             475             480
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Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
            485             490             495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
            500             505             510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
            515             520             525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
    530             535             540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545             550             555             560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
            565             570             575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
            580             585             590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
            595             600             605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
    610             615             620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625             630             635             640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
            645             650             655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
            660             665             670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
            675             680             685

Phe Phe Glu Gln Met Gln Asn
    690             695


<210> 11
<211> 2088
<212> DNA
<213> Homo sapiens

<400> 11
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-18-

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cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga      120

ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa      180

acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg      240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg      300

ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt      360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg      420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag      480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga      540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat      600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg      660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa      720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa      780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca      840

gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt      900

gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa      960

gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag     1020

gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc     1080

caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag     1140

acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaac     1200

tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag     1260

aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg     1320

cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt     1380

gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc     1440

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tctgggttga caaatatcaa gacggaggag atctctgaag tgaatctgga tgcagaattc     1800

cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg     1860

ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgtcat agcgacagtg     1920

atcgtcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg     1980
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gtggaggttg acgccgctgt cacccccagag gagcgccacc tgtccaagat gcagcagaac   2040

ggctacgaaa atccaaccta caagttctttt gagcagatgc agaactag   2088

<210> 12
<211> 695
<212> PRT
<213> Homo sapiens

<400> 12

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1   5   10   15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20   25   30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
            35   40   45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50   55   60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65   70   75   80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85   90   95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
            100   105   110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
            115   120   125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
    130   135   140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145   150   155   160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165   170   175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
            180   185   190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
            195   200   205

-20-

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210   215   220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225   230   235   240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
                245   250   255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
                260   265   270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
        275   280   285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
    290   295   300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305   310   315   320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
            325   330   335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
            340   345   350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
        355   360   365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
    370   375   380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385   390   395   400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
            405   410   415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
            420   425   430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
    435   440   445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
    450   455   460

-21-

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465   470   475   480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
                485   490   495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
            500   505   510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
            515   520   525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
        530   535   540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545   550   555   560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
            565   570   575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
            580   585   590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
            595   600   605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
    610   615   620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625   630   635   640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
            645   650   655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
            660   665   670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
            675   680   685

Phe Phe Glu Gln Met Gln Asn
690   695

-22-

<210> 13
<211> 2088
<212> DNA
<213> Homo sapiens

<400> 13
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa   180

acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg   240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg   300

ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt   360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg   420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag   480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga   540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat   600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg   660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa   720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa   780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca   840

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gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa   960

gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atggaagag   1020

gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc   1080

caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag   1140

acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaac   1200

tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag   1260

aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg   1320

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gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac   1680

gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt   1740

-23-

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cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg   1860

ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgtcat agcgacagtg   1920

atcttcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg   1980

gtggaggttg acgccgctgt cacccccagag gagcgccacc tgtccaagat gcagcagaac   2040

ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag              2088
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<210> 14
<211> 695
<212> PRT
<213> Homo sapiens

<400> 14

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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20                  25                  30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
            35                  40                  45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50                  55                  60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65                  70                  75                  80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85                  90                  95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
            100                 105                 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
            115                 120                 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
        130                 135                 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145                 150                 155                 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165                 170                 175
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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
        180             185             190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
        195             200             205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210             215             220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225             230             235             240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
                245             250             255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
            260             265             270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
        275             280             285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
    290             295             300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305             310             315             320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
            325             330             335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
        340             345             350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
        355             360             365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
    370             375             380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385             390             395             400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
            405             410             415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
        420             425             430
```

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Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
        435   440   445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
        450   455   460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465   470   475   480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
                485   490   495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
        500   505   510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
        515   520   525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530   535   540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545   550   555   560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
                565   570   575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
                580   585   590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
        595   600   605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
        610   615   620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625   630   635   640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
        645   650   655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
        660   665   670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
        675   680   685

Phe Phe Glu Gln Met Gln Asn
     690   695

<210> 15
<211> 2094
<212> DNA
<213> Homo sapiens

<400> 15
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa   180

acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg   240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg   300

ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt   360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg   420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag   480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga   540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat   600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg   660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa   720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa   780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca   840

gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt   900

gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa   960

gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag   1020

gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc   1080

caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag   1140

acacacatgg ccagagtgga agccatgctc aatgaccgcc gcgcctggc cctggagaac   1200

tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag   1260

aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg   1320

cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt   1380

gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc   1440

gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaacta ttcagatgac   1500

gtcttggcca acatgattag tgaaccaagg atcagttacg aaacgatgc tctcatgcca   1560

tctttgaccg aaacgaaaac caccgtggag ctccttcccg tgaatggaga gttcagcctg   1620

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gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac    1680

gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt    1740

tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc    1800

cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg    1860

ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgtcat agcgacagtg    1920

atcgtcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg    1980

gtggaggttg acgccgctgt caccccagag gagcgccacc tgtccaagat gcagcagaac    2040

ggctacgaaa atccaaccta caagttcttt gagcagatgc agaacaagaa gtag          2094
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<210> 16
<211> 697
<212> PRT
<213> Homo sapiens

<400> 16

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Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1                   5                   10                  15


Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
                20                  25                  30


Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
            35                  40                  45


Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50                  55                  60


Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65                  70                  75                  80


Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85                  90                  95


Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
                100                 105                 110


Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
            115                 120                 125


Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
        130                 135                 140


Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145                 150                 155                 160
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Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165   170   175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
                180   185   190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
                195   200   205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210   215   220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225   230   235   240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
                245   250   255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
                260   265   270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
                275   280   285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290   295   300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305   310   315   320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
                325   330   335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
                340   345   350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
                355   360   365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
                370   375   380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385   390   395   400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
                405   410   415

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Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
           420   425   430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
        435   440   445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
      450   455   460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465   470   475   480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
          485   490   495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
        500   505   510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
        515   520   525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
        530   535   540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545   550   555   560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
          565   570   575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
        580   585   590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
        595   600   605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
      610   615   620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625   630   635   640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
        645   650   655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
      660   665   670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
    675   680   685

Phe Phe Glu Gln Met Gln Asn Lys Lys
    690   695

<210> 17
<211> 2094
<212> DNA
<213> Homo sapiens

<400> 17
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa   180
acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg   240
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg   300
ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt   360
gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg   420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag   480
aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga   540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat   600
gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg   660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa   720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa   780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca   840
gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt   900
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa   960
gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag  1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc  1080
caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag  1140
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tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag  1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg  1320
cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt  1380
gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc  1440
gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaacta ttcagatgac  1500
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tctttgaccg aaacgaaaac caccgtggag ctccttcccg tgaatggaga gttcagcctg   1620

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gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt   1740

tctgggttga caaatatcaa gacggaggag atctctgaag tgaatctgga tgcagaattc   1800

cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg   1860

ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgtcat agcgacagtg   1920

atcgtcatca ccttggtgat gctgaagaag aaacagtaca tccattca tcatggtgtg     1980

gtggaggttg acgccgctgt cacccagag gagcgccacc tgtccaagat gcagcagaac     2040

ggctacgaaa atccaaccta caagttcttt gagcagatgc agaacaagaa gtag          2094
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<210> 18
<211> 697
<212> PRT
<213> Homo sapiens

<400> 18

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Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1               5                   10                  15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20                  25                  30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
            35                  40                  45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50                  55                  60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65                  70                  75                  80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85                  90                  95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
            100                 105                 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
            115                 120                 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
        130                 135                 140
```

-32-

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145   150   155   160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                 165   170   175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
             180   185   190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
             195   200   205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
    210   215   220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225   230   235   240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
                 245   250   255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
             260   265   270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
    275   280   285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
    290   295   300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305   310   315   320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
             325   330   335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
             340   345   350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
             355   360   365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
    370   375   380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385   390   395   400

-33-

```
Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
             405                 410             415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
             420                 425             430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
             435                 440             445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
             450                 455             460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465                 470                 475             480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
                 485                 490             495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
             500                 505             510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
             515                 520             525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
    530                 535                 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545                 550                 555             560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
             565                 570             575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
             580                 585             590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
             595                 600             605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
             610                 615             620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625                 630                 635             640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
             645                 650             655
```

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His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
                660   665   670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
                675   680   685

Phe Phe Glu Gln Met Gln Asn Lys Lys
            690   695

<210> 19
<211> 2094
<212> DNA
<213> Homo sapiens

<400> 19
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa   180

acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg   240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg   300

ggccgcaagc agtgcaagac ccatcccac ttgtgattc cctaccgctg cttagttggt   360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg   420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag   480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga   540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat   600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg   660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa   720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa   780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca   840

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gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa   960

gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag   1020

gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc   1080

caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag   1140

acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaac   1200

tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag   1260

aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg   1320

cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt   1380

-35-

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gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc    1440

gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaacta ttcagatgac    1500

gtcttggcca acatgattag tgaaccaagg atcagttacg aaacgatgc tctcatgcca      1560

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cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg    1860

ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgtcat agcgacagtg    1920

atcttcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg    1980

gtggaggttg acgccgctgt caccccagag gagcgccacc tgtccaagat gcagcagaac    2040

ggctacgaaa atccaaccta caagttcttt gagcagatgc agaacaagaa gtag           2094
```

<210>   20
<211>   697
<212>   PRT
<213>   Homo sapiens

<400> 20

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Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1               5                   10                  15


Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20                  25                  30


Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
        35                  40                  45


Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
    50                  55                  60


Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65                  70                  75                  80


Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85                  90                  95


Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
            100                 105                 110


Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
            115                 120                 125
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Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
    130             135             140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145             150             155             160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
            165             170             175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
        180             185             190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
        195             200             205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
    210             215             220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225             230             235             240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
            245             250             255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
        260             265             270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
    275             280             285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
    290             295             300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305             310             315             320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
            325             330             335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
        340             345             350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
        355             360             365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
    370             375             380
```

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Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385   390   395   400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
            405   410   415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
            420   425   430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
        435   440   445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
    450   455   460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465   470   475   480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
            485   490   495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
        500   505   510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
        515   520   525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
    530   535   540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545   550   555   560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
            565   570   575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
        580   585   590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
        595   600   605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
    610   615   620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625   630   635   640

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```
Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
            645             650             655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
            660             665             670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
            675             680             685

Phe Phe Glu Gln Met Gln Asn Lys Lys
    690             695
```

```
<210>   21
<211>   1341
<212>   DNA
<213>   Homo sapiens

<400>   21
atggctagca tgactggtgg acagcaaatg ggtcgcggat ccacccagca cggcatccgg      60

ctgcccctgc gcagcggcct ggggggcgcc cccctggggc tgcggctgcc ccgggagacc     120

gacgaagagc ccgaggagcc cggccggagg ggcagctttg tggagatggt ggacaacctg     180

aggggcaagt cggggcaggg ctactacgtg gagatgaccg tgggcagccc cccgcagacg     240

ctcaacatcc tggtggatac aggcagcagt aactttgcag tgggtgctgc ccccacccc      300

ttcctgcatc gctactacca gaggcagctg tccagcacat accgggacct ccggaagggt     360

gtgtatgtgc cctacaccca gggcaagtgg gaagggagc tgggcaccga cctggtaagc     420

atcccccatg gccccaacgt cactgtgcgt gccaacattg ctgccatcac tgaatcagac     480

aagttcttca tcaacggctc caactgggaa ggcatcctgg ggctggccta tgctgagatt     540

gccaggcctg acgactccct ggagcctttc tttgactctc tggtaaagca gacccacgtt     600

cccaacctct ctccctgca cctttgtggt gctggcttcc ccctcaacca gtctgaagtg     660

ctggcctctg tcggagggag catgatcatt ggaggtatcg accactcgct gtacacaggc     720

agtctctggt atacacccat ccggcgggag tggtattatg aggtcatcat tgtgcgggtg     780

gagatcaatg acaggatct gaaaatggac tgcaaggagt acaactatga caagagcatt     840

gtggacagtg gcaccaccaa ccttcgtttg cccaagaaag tgtttgaagc tgcagtcaaa     900

tccatcaagg cagcctcctc cacggagaag ttccctgatg gtttctggct aggagagcag     960

ctggtgtgct ggcaagcagg caccaccct tggaacattt cccagtcat ctcactctac    1020

ctaatgggtg aggttaccaa ccagtccttc cgcatcacca tccttccgca gcaatacctg    1080

cggccagtgg aagatgtggc cacgtcccaa gacgactgtt acaagtttgc catctcacag    1140

tcatccacgg gcactgttat gggagctgtt atcatggagg cttctacgt tgtctttgat    1200

cgggcccgaa aacgaattgg ctttgctgtc agcgcttgcc atgtgcacga tgagttcagg    1260
```

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acggcagcgg tggaaggccc ttttgtcacc ttggacatgg aagactgtgg ctacaacatt   1320

ccacagacag atgagtcatg a   1341

<210>   22
<211>   446
<212>   PRT
<213>   Homo sapiens

<400>   22

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Thr Gln
1   5   10   15

His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu
            20   25   30

Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly
            35   40   45

Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser
    50   55   60

Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr
65   70   75   80

Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala
                85   90   95

Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser
            100   105   110

Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly
            115   120   125

Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly
    130   135   140

Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp
145   150   155   160

Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala
                165   170   175

Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp
            180   185   190

Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu
            195   200   205

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```
Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val
    210             215             220

Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly
225             230             235             240

Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile
            245             250             255

Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys
        260             265             270

Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu
    275             280             285

Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala
    290             295             300

Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln
305             310             315             320

Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val
            325             330             335

Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile
            340             345             350

Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr
            355             360             365

Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly
    370             375             380

Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp
385             390             395             400

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His
            405             410             415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp
            420             425             430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
    435             440             445
```

<210> 23
<211> 1380
<212> DNA
<213> Homo sapiens

<400> 23
atggctagca tgactggtgg acagcaaatg ggtcgcggat cgatgactat ctctgactct   60

ccgcgtgaac aggacggatc cacccagcac ggcatccggc tgcccctgcg cagcggcctg   120

gggggcgccc ccctggggct gcggctgccc cgggagaccg acgaagagcc cgaggagccc   180

ggccggaggg gcagctttgt ggagatggtg gacaacctga ggggcaagtc ggggcagggc   240

tactacgtgg agatgaccgt gggcagcccc ccgcagacgc tcaacatcct ggtggataca   300

ggcagcagta actttgcagt gggtgctgcc ccccacccct tcctgcatcg ctactaccag   360

aggcagctgt ccagcacata ccgggacctc cggaagggtg tgtatgtgcc ctacacccag   420

ggcaagtggg aagggggagct gggcaccgac ctggtaagca tcccccatgg ccccaacgtc   480

actgtgcgtg ccaacattgc tgccatcact gaatcagaca agttcttcat caacggctcc   540

aactgggaag gcatcctggg gctggcctat gctgagattg ccaggcctga cgactccctg   600

gagcctttct ttgactctct ggtaaagcag acccacgttc ccaacctctt ctccctgcac   660

ctttgtggtg ctggcttccc cctcaaccag tctgaagtgc tggcctctgt cggagggagc   720

atgatcattg aggtatcga ccactcgctg tacacaggca gtctctggta tacacccatc   780

cggcgggagt ggtattatga ggtcatcatt gtgcgggtgg agatcaatgg acaggatctg   840

aaaatggact gcaaggagta caactatgac aagagcattg tggacagtgg caccaccaac   900

cttcgtttgc ccaagaaagt gtttgaagct gcagtcaaat ccatcaaggc agcctcctcc   960

acggagaagt tccctgatgg tttctggcta ggagagcagc tggtgtgctg gcaagcaggc   1020

accacccctt ggaacatttt cccagtcatc tcactctacc taatgggtga ggttaccaac   1080

cagtccttcc gcatcaccat ccttccgcag caatacctgc ggccagtgga agatgtggcc   1140

acgtcccaag acgactgtta caagtttgcc atctcacagt catccacggg cactgttatg   1200

ggagctgtta tcatggaggg cttctacgtt gtctttgatc gggcccgaaa acgaattggc   1260

tttgctgtca gcgcttgcca tgtgcacgat gagttcagga cggcagcggt ggaaggccct   1320

tttgtcacct tggacatgga agactgtggc tacaacattc cacagacaga tgagtcatga   1380

<210> 24
<211> 459
<212> PRT
<213> Homo sapiens

<400> 24

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1   5   10   15

```
Ile Ser Asp Ser Pro Arg Glu Gln Asp Gly Ser Thr Gln His Gly Ile
            20              25              30

Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg
            35              40              45

Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly
    50              55              60

Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly
65              70              75              80

Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile
            85              90              95

Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His
            100             105             110

Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg
        115             120             125

Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu
    130             135             140

Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val
145             150             155             160

Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe
            165             170             175

Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu
            180             185             190

Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val
            195             200             205

Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala
    210             215             220

Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser
225             230             235             240

Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp
            245             250             255

Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg
            260             265             270
```

```
Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn
        275                 280                 285


Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro
        290                 295                 300


Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser
305                 310                 315                 320


Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys
                325                 330                 335


Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu
                340                 345                 350


Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu
        355                 360                 365


Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp
        370                 375                 380


Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met
385                 390                 395                 400


Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg
                405                 410                 415


Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe
                420                 425                 430


Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
        435                 440                 445


Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
    450                 455


<210>   25
<211>   1302
<212>   DNA
<213>   Homo sapiens

<400>   25
atgactcagc atggtattcg tctgccactg cgtagcggtc tgggtggtgc tccactgggt      60

ctgcgtctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt     120

gtggagatgg tggacaacct gaggggcaag tcggggcagg ctactacgt ggagatgacc      180

gtgggcagcc ccccgcagac gctcaacatc ctggtggata caggcagcag taactttgca     240

gtgggtgctg cccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca     300
```

```
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag      360

ctgggcaccg acctggtaag catcccccat ggccccaacg tcactgtgcg tgccaacatt      420

gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg      480

gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct      540

ctggtaaagc agacccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc      600

cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggtatc      660

gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat      720

gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag      780

tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa      840

gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat      900

ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt      960

ttcccagtca tctcactcta cctaatgggt gaggttacca accagtcctt ccgcatcacc     1020

atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt     1080

tacaagtttg ccatctcaca gtcatccacg ggcactgtta tgggagctgt tatcatggag     1140

ggcttctacg ttgtctttga tcgggcccga aaacgaattg ctttgctgt cagcgcttgc      1200

catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg     1260

gaagactgtg gctacaacat tccacagaca gatgagtcat ga                        1302
```

<210> 26
<211> 433
<212> PRT
<213> Homo sapiens

<400> 26

```
Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly
1               5                   10                  15


Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu
                20                  25                  30


Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg
                35                  40                  45


Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro
    50                  55                  60


Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala
65                  70                  75                  80
```

```
Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln
                85              90                  95

Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
            100             105             110

Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
        115             120             125

Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
    130             135             140

Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
145             150             155             160

Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro
            165             170             175

Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
            180             185             190

Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
        195             200             205

Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu
    210             215             220

Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr
225             230             235             240

Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met
            245             250             255

Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr
            260             265             270

Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser
        275             280             285

Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu
    290             295             300

Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile
305             310             315             320

Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser
            325             330             335
```

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```
Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp
        340             345             350

Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser
        355             360             365

Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val
        370             375             380

Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys
385             390             395             400

His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val
                405             410             415

Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
            420             425             430

Ser
```

```
<210>   27
<211>   1278
<212>   DNA
<213>   Homo sapiens

<400>   27
atggctagca tgactggtgg acagcaaatg ggtcgcggat cgatgactat ctctgactct   60

ccgctggact ctggtatcga aaccgacgga tcctttgtgg agatggtgga caacctgagg   120

ggcaagtcgg ggcagggcta ctacgtggag atgaccgtgg gcagcccccc gcagacgctc   180

aacatcctgg tggatacagg cagcagtaac tttgcagtgg gtgctgcccc ccacccttc    240

ctgcatcgct actaccagag gcagctgtcc agcacatacc gggacctccg gaagggtgtg   300

tatgtgccct acacccaggg caagtgggaa ggggagctgg gcaccgacct ggtaagcatc   360

ccccatggcc ccaacgtcac tgtgcgtgcc aacattgctg ccatcactga atcagacaag   420

ttcttcatca cggctccaa ctgggaaggc atcctggggc tggcctatgc tgagattgcc    480

aggcctgacg actccctgga gcctttcttt gactctctgg taaagcagac ccacgttccc   540

aacctcttct ccctgcacct ttgtggtgct ggcttccccc tcaaccagtc tgaagtgctg   600

gcctctgtcg gagggagcat gatcattgga ggtatcgacc actcgctgta cacaggcagt   660

ctctggtata cacccatccg gcgggagtgg tattatgagg tcatcattgt gcgggtggag   720

atcaatggac aggatctgaa aatggactgc aaggagtaca actatgacaa gagcattgtg   780

gacagtggca ccaccaacct tcgtttgccc aagaaagtgt ttgaagctgc agtcaaatcc   840

atcaaggcag cctcctccac ggagaagttc cctgatggtt tctggctagg agagcagctg   900
```

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```
gtgtgctggc aagcaggcac cacccccttgg aacattttcc cagtcatctc actctaccta     960

atgggtgagg ttaccaacca gtccttccgc atcaccatcc ttccgcagca atacctgcgg    1020

ccagtggaag atgtggccac gtcccaagac gactgttaca agtttgccat ctcacagtca    1080

tccacgggca ctgttatggg agctgttatc atggagggct tctacgttgt ctttgatcgg    1140

gcccgaaaac gaattggctt tgctgtcagc gcttgccatg tgcacgatga gttcaggacg    1200

gcagcggtgg aaggcccttt tgtcaccttg gacatggaag actgtggcta caacattcca    1260

cagacagatg agtcatga                                                  1278
```

<210> 28
<211> 425
<212> PRT
<213> Homo sapiens

<400> 28

```
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1               5                   10                  15

Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe
            20                  25                  30

Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr
        35                  40                  45

Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val
    50                  55                  60

Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe
65                  70                  75                  80

Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu
                85                  90                  95

Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu
            100                 105                 110

Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val
            115                 120                 125

Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn
    130                 135                 140

Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala
145                 150                 155                 160
```

Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln
            165   170   175

Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe
            180   185   190

Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile
            195   200   205

Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr
    210   215   220

Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu
225   230   235   240

Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp
            245   250   255

Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys
            260   265   270

Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu
            275   280   285

Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln
    290   295   300

Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu
305   310   315   320

Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln
            325   330   335

Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys
            340   345   350

Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala
            355   360   365

Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg
    370   375   380

Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr
385   390   395   400

Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly
            405   410   415

Tyr Asn Ile Pro Gln Thr Asp Glu Ser
          420   425

<210>   29
<211>   1362
<212>   DNA
<213>   Homo sapiens

<400>   29
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ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc ccccctgggg   120

ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt   180

gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc   240

gtgggcagcc ccccgcagac gctcaacatc ctggtggata caggcagcag taactttgca   300

gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca   360

taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag   420

ctgggcaccg acctggtaag catcccccat ggccccaacg tcactgtgcg tgccaacatt   480

gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg   540

gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct   600

ctggtaaagc agacccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc   660

cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggtatc   720

gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat   780

gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag   840

tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa   900

gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat   960

ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt   1020

ttcccagtca tctcactcta cctaatgggt gaggttacca accagtcctt ccgcatcacc   1080

atccttccgc agcaatacct gcggccagtg aagatgtgg ccacgtccca agacgactgt   1140

tacaagtttg ccatctcaca gtcatccacg ggcactgtta tgggagctgt tatcatggag   1200

ggcttctacg ttgtctttga tcgggcccga aaacgaattg ctttgctgt cagcgcttgc   1260

catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg   1320

gaagactgtg gctacaacat tccacagaca gatgagtcat ga   1362

<210>   30
<211>   453
<212>   PRT
<213>   Homo sapiens

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<400> 30

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1   5   10   15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
            20   25   30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
        35   40   45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
    50   55   60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65   70   75   80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
            85   90   95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
            100   105   110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115   120   125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
    130   135   140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145   150   155   160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
            165   170   175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
            180   185   190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
        195   200   205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
    210   215   220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225   230   235   240

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```
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
                245                 250                 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
            260                 265                 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
            275                 280                 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
    290                 295                 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305                 310                 315                 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
                325                 330                 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
            340                 345                 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
            355                 360                 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
    370                 375                 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385                 390                 395                 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
            405                 410                 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
            420                 425                 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
        435                 440                 445

Gln Thr Asp Glu Ser
    450


<210>   31
<211>   1380
<212>   DNA
<213>   Homo sapiens
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<400> 31
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atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgct gcctgcccac    60
ggcacccagc acggcatccg gctgcccctg cgcagcggcc tgggggggcgc ccccctgggg   120
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt   180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc   240
gtgggcagcc ccccgcagac gctcaacatc ctggtggata caggcagcag taactttgca   300
gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca   360
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaagggggag   420
ctgggcaccg acctggtaag catcccccat ggccccaacg tcactgtgcg tgccaacatt   480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg   540
gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct   600
ctggtaaagc agacccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc   660
cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggtatc   720
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat   780
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag   840
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa   900
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat   960
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc cttggaacatt  1020
ttcccagtca tctcactcta cctaatgggt gaggttacca accagtcctt ccgcatcacc  1080
atccttccgc agcaatacct gcggccagtg aagatgtgg ccacgtccca agacgactgt  1140
tacaagtttg ccatctcaca gtcatccacg ggcactgtta tgggagctgt tatcatggag  1200
ggcttctacg ttgtctttga tcgggcccga aaacgaattg gctttgctgt cagcgcttgc  1260
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg  1320
gaagactgtg gctacaacat tccacagaca gatgagtcac agcagcagca gcagcagtga  1380
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<210>   32
<211>   459
<212>   PRT
<213>   Homo sapiens

<400>   32

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Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1                5                   10                  15


Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
                20                  25                  30
```

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Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
        35   40   45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
    50   55   60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65   70   75   80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
            85   90   95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
        100   105   110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115   120   125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
    130   135   140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145   150   155   160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
            165   170   175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
        180   185   190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
        195   200   205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210   215   220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225   230   235   240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
            245   250   255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
        260   265   270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
    275   280   285

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Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
    290   295   300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305   310   315   320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
                325   330   335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
                340   345   350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
            355   360   365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
    370   375   380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385   390   395   400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
                405   410   415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
                420   425   430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
                435   440   445

Gln Thr Asp Glu Ser His His His His His His
    450   455

<210> 33
<211> 25
<212> PRT
<213> Homo sapiens

<400> 33

Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu
1   5   10   15

Ser Ser Leu Val Arg His Arg Trp Lys
                20   25

<210> 34
<211> 19
<212> PRT
<213> Homo sapiens

<400> 34

Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser
1   5   10   15

Leu Leu Lys

<210>   35
<211>   29
<212>   DNA
<213>   Homo sapiens

<400>   35
gtggatccac ccagcacggc atccggctg   29

<210>   36
<211>   36
<212>   DNA
<213>   Homo sapiens

<400>   36
gaaagctttc atgactcatc tgtctgtgga atgttg   36

<210>   37
<211>   39
<212>   DNA
<213>   Homo sapiens

<400>   37
gatcgatgac tatctctgac tctccgcgtg aacaggacg   39

<210>   38
<211>   39
<212>   DNA
<213>   Homo sapiens

<400>   38
gatccgtcct gttcacgcgg agagtcagag atagtcatc   39

<210>   39
<211>   77
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Hu-Asp2

<400>   39
cggcatccgg ctgcccctgc gtagcggtct gggtggtgct ccactgggtc tgcgtctgcc 60

ccgggagacc gacgaag   77

<210> 40
<211> 77
<212> DNA
<213> Artificial sequence

<220>
<223> Hu-Asp2

<400> 40
cttcgtcggt ctcccggggc agacgcagac ccagtggagc accacccaga ccgctacgca   60

ggggcagccg gatgccg   77

<210> 41
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Caspase-8 Cleavage Site

<400> 41
gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g   51

<210> 42
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Caspase-8 Cleavage Site

<400> 42
gatccgtcgg tttcgatacc agagtccagc ggagagtcag agatagtcat c   51

<210> 43
<211> 32
<212> DNA
<213> Homo sapiens

<400> 43
aaggatcctt tgtggagatg gtggacaacc tg   32

<210> 44
<211> 36
<212> DNA
<213> Homo sapiens

<400> 44
gaaagctttc atgactcatc tgtctgtgga atgttg   36

<210> 45
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> 6-His tag

<400> 45
gatcgcatca tcaccatcac catg   24

<210> 46
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> 6-His tag

<400> 46
gatccatggt gatggtgatg atgc   24

<210> 47
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 47
gactgaccac tcgaccaggt tc   22

<210> 48
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 48
cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c   51

<210> 49
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 49
cgaattaaat tccagcacac tggcta   26

<210> 50
<211> 1287
<212> DNA
<213> Artificial sequence

<220>
<223> Hu-Asp2(b) delta TM

<400> 50

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atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgct gcctgcccac      60

ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctgggg      120

ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt     180

gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc     240

gtgggcagcc ccccgcagac gctcaacatc ctggtggata caggcagcag taactttgca    300

gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca     360

taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag     420

ctgggcaccg acctggtaag catcccccat ggccccaacg tcactgtgcg tgccaacatt     480

gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg     540

gggctggcct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct     600

gaagtgctgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac     660

acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt catcattgtg     720

cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag     780

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gtcaaatcca tcaaggcagc ctcctccacg gagaagttcc ctgatggttt ctggctagga     900

gagcagctgg tgtgctggca agcaggcacc accccttgga acattttccc agtcatctca     960

ctctacctaa tgggtgaggt taccaaccag tccttccgca tcaccatcct tccgcagcaa    1020

tacctgcggc cagtggaaga tgtggccacg tcccaagacg actgttacaa gtttgccatc   1080

tcacagtcat ccacgggcac tgttatggga gctgttatca tggagggctt ctacgttgtc    1140

tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag    1200

ttcaggacgg cagcggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac    1260

aacattccac agacagatga gtcatga                                       1287
```

<210> 51
<211> 428
<212> PRT
<213> Artificial sequence

<220>
<223> Hu-Asp2(b) delta TM

<400> 51

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Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1               5                   10                  15


Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
            20                  25                  30
```

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```
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
        35                  40                  45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
    50              55                  60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65              70                  75                      80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
            85                  90                  95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
            100             105             110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115             120             125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
    130             135             140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145             150             155             160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
            165             170             175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
        180             185             190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
        195             200             205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
    210             215             220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
225             230             235             240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
            245             250             255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
        260             265             270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
    275             280             285
```

```
Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
    290             295             300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
305             310             315             320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
                325             330             335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
            340             345             350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
        355             360             365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
    370             375             380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385             390             395             400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
            405             410             415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
        420             425
```

<210> 52
<211> 1305
<212> DNA
<213> Artificial sequence

<220>
<223> Hu-Asp2(b) delta TM

<400> 52
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atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgct gcctgcccac    60

ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc ccccctgggg   120

ctgcggctgc ccgggagac  cgacgaagag cccgaggagc ccggccggag gggcagcttt   180

gtggagatgg tggacaacct gaggggcaag tcggggcagg ctactacgt  ggagatgacc   240

gtgggcagcc ccccgcagac gctcaacatc ctggtggata caggcagcag taactttgca   300

gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca   360

taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaagggggag   420

ctgggcaccg acctggtaag catcccccat ggccccaacg tcactgtgcg tgccaacatt   480

gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg   540
```

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```
gggctggcct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct      600

gaagtgctgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac      660

acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt catcattgtg      720

cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag      780

agcattgtgg acagtggcac caccaacctt cgtttgccca agaaagtgtt tgaagctgca      840

gtcaaatcca tcaaggcagc ctcctccacg gagaagttcc ctgatggttt ctggctagga      900

gagcagctgg tgtgctggca agcaggcacc accccttgga acattttccc agtcatctca      960

ctctacctaa tgggtgaggt taccaaccag tccttccgca tcaccatcct tccgcagcaa     1020

tacctgcggc cagtggaaga tgtggccacg tcccaagacg actgttacaa gtttgccatc     1080

tcacagtcat ccacgggcac tgttatggga gctgttatca tggagggctt ctacgttgtc     1140

tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag     1200

ttcaggacgg cagcggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac     1260

aacattccac agacagatga gtcacagcag cagcagcagc agtga                     1305


<210>  53
<211>  434
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Hu-Asp2(b) delta TM

<400>  53

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1               5                   10                  15


Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
            20                  25                  30


Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
            35                  40                  45


Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
    50                  55                  60


Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65                  70                  75                  80


Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
                85                  90                  95


Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
                100                 105                 110
```

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Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115   120   125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
    130   135   140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145   150   155   160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
                165   170   175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
                180   185   190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
            195   200   205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
    210   215   220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
225   230   235   240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
                245   250   255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
            260   265   270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
        275   280   285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
    290   295   300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
305   310   315   320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
                325   330   335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
            340   345   350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
            355   360   365

-63-

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
    370   375   380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385   390   395   400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
            405   410   415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His
            420   425   430

His His

<210> 54
<211> 2310
<212> DNA
<213> Homo sapiens

<400> 54
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cccactgatg gtaatgctgg cctgctggct gaacccaga ttgccatgtt ctgtggcaga   120

ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa   180

acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg   240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg   300

ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt   360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg   420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag   480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga   540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat   600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg   660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa   720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa   780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca   840

gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc   900

cgagcaatga tctcccgctg gtactttgat gtgactgaag ggaagtgtgc cccattcttt   960

tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg   1020

tgtggcagcg ccatgtccca aagtttactc aagactaccc aggaacctct tggccgagat   1080

-64-

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cctgttaaac ttcctacaac agcagccagt acccctgatg ccgttgacaa gtatctcgag    1140

acacctgggg atgagaatga acatgcccat ttccagaaag ccaaagagag gcttgaggcc    1200

aagcaccgag agagaatgtc ccaggtcatg agagaatggg aagaggcaga acgtcaagca    1260

aagaacttgc ctaaagctga taagaaggca gttatccagc atttccagga ·gaaagtggaa   1320

tctttggaac aggaagcagc caacgagaga cagcagctgg tggagacaca catggccaga    1380

gtggaagcca tgctcaatga ccgccgccgc ctggccctgg agaactacat caccgctctg    1440

caggctgttc ctcctcggcc tcgtcacgtg ttcaatatgc taaagaagta tgtccgcgca    1500

gaacagaagg acagacagca caccctaaag catttcgagc atgtgcgcat ggtggatccc    1560

aagaaagccg ctcagatccg gtcccaggtt atgacacacc tccgtgtgat ttatgagcgc    1620

atgaatcagt ctctctccct gctctacaac gtgcctgcag tggccgagga gattcaggat    1680

gaagttgatg agctgcttca gaaagagcaa aactattcag atgacgtctt ggccaacatg    1740

attagtgaac caaggatcag ttacggaaac gatgctctca tgccatcttt gaccgaaacg    1800

aaaaccaccg tggagctcct tcccgtgaat ggagagttca gcctggacga tctccagccg    1860

tggcattctt ttggggctga ctctgtgcca gccaacacag aaaacgaagt tgagcctgtt    1920

gatgcccgcc ctyctgccga ccgaggactg accactcgac caggttctgg gttgacaaat    1980

atcaagacgg aggagatctc tgaagtgaag atggatgcag aattccgaca tgactcagga    2040

tatgaagttc atcatcaaaa attggtgttc tttgcagaag atgtgggttc aaacaaaggt    2100

gcaatcattg gactcatggt gggcggtgtt gtcatagcga cagtgatcgt catcaccttg    2160

gtgatgctga agaagaaaca gtacacatcc attcatcatg gtgtggtgga ggttgacgcc    2220

gctgtcaccc cagaggagcg ccacctgtcc aagatgcagc agaacggcta cgaaaatcca    2280

acctacaagt tctttgagca gatgcagaac                                     2310
```

<210> 55
<211> 770
<212> PRT
<213> Homo sapiens

<400> 55

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Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1           5               10              15


Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20              25              30


Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
        35              40              45
```

-65-

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
    50   55   60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65   70   75   80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
            85   90   95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
            100   105   110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
        115   120   125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
    130   135   140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145   150   155   160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
            165   170   175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
        180   185   190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
    195   200   205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210   215   220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225   230   235   240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
            245   250   255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
            260   265   270

Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
        275   280   285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
    290   295   300

-66-

```
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305             310             315                         320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
                325             330                 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
            340             345                 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
        355             360             365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
    370             375             380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385             390             395                         400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
            405             410             415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
        420             425             430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
        435             440             445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
    450             455             460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465             470             475                         480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
            485             490             495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
        500             505             510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
        515             520             525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
    530             535             540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545             550             555                         560
```

-67-

```
Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
            565             570                 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
            580             585             590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
            595             600             605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
    610             615             620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625             630             635             640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
            645             650             655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
            660             665             670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
            675             680             685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
    690             695             700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705             710             715             720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
            725             730             735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
            740             745             750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
            755             760             765

Gln Asn
770


<210>  56
<211>  2253
<212>  DNA
<213>  Homo sapiens
```

<400> 56

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa     180

acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg     240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg     300

ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt     360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg     420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag     480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga     540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat     600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg     660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa     720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa     780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca     840

gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc     900

cgagcaatga tctcccgctg gtactttgat gtgactgaag ggaagtgtgc cccattcttt     960

tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg    1020

tgtggcagcg ccattcctac aacagcagcc agtacccctg atgccgttga caagtatctc    1080

gagacacctg gggatgagaa tgaacatgcc catttccaga aagccaaaga gaggcttgag    1140

gccaagcacc gagagagaat gtcccaggtc atgagagaat gggaagaggc agaacgtcaa    1200

gcaaagaact tgcctaaagc tgataagaag gcagttatcc agcatttcca ggagaaagtg    1260

gaatctttgg aacaggaagc agccaacgag agacagcagc tggtggagac acacatggcc    1320

agagtggaag ccatgctcaa tgaccgccgc cgcctggccc tggagaacta catcaccgct    1380

ctgcaggctg ttcctcctcg gcctcgtcac gtgttcaata tgctaaagaa gtatgtccgc    1440

gcagaacaga aggacagaca gcacaccta aagcatttcg agcatgtgcg catggtggat    1500

cccaagaaag ccgctcagat ccggtcccag gttatgacac acctccgtgt gatttatgag    1560

cgcatgaatc agtctctctc cctgctctac aacgtgcctg cagtggccga ggagattcag    1620

gatgaagttg atgagctgct tcagaaagag caaaactatt cagatgacgt cttggccaac    1680

atgattagtg aaccaaggat cagttacgga aacgatgctc tcatgccatc tttgaccgaa    1740

acgaaaacca ccgtggagct ccttcccgtg aatggagagt tcagcctgga cgatctccag    1800

ccgtggcatt cttttggggc tgactctgtg ccagccaaca cagaaaacga agttgagcct    1860
```

-69-

```
gttgatgccc gccctgctgc cgaccgagga ctgaccactc gaccaggttc tgggttgaca      1920

aatatcaaga cggaggagat ctctgaagtg aagatggatg cagaattccg acatgactca      1980

ggatatgaag ttcatcatca aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa      2040

ggtgcaatca ttggactcat ggtgggcggt gttgtcatag cgacagtgat cgtcatcacc      2100

ttggtgatgc tgaagaagaa acagtacaca tccattcatc atggtgtggt ggaggttgac      2160

gccgctgtca ccccagagga gcgccacctg tccaagatgc agcagaacgg ctacgaaaat      2220

ccaacctaca agttctttga gcagatgcag aac                                   2253
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<210> 57
<211> 751
<212> PRT
<213> Homo sapiens

<400> 57

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Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1               5                   10                  15


Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20                  25                  30


Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
            35                  40                  45


Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50                  55                  60


Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65                  70                  75                  80


Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85                  90                  95


Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
            100                 105                 110


Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
            115                 120                 125


Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
        130                 135                 140


Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145                 150                 155                 160
```

-70-
```

```
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165             170                 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
            180             185             190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
            195             200             205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210             215             220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225             230             235             240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
            245             250             255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
            260             265             270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
        275             280             285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
    290             295             300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305             310             315             320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
            325             330             335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
        340             345             350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
        355             360             365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
    370             375             380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
385             390             395             400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
            405             410             415
```

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
        420   425   430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
        435   440   445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
    450   455   460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
465   470   475   480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
            485   490   495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
        500   505   510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
        515   520   525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
    530   535   540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
545   550   555   560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
            565   570   575

Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
        580   585   590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
        595   600   605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
        610   615   620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
625   630   635   640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
            645   650   655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
            660   665   670

-72-

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Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
        675                 680                 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
        690                 695                 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705                 710                 715                 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
                725             730             735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn
            740                 745             750


<210>  58
<211>  2316
<212>  DNA
<213>  Homo sapiens

<400>  58
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa     180

acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg     240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg     300

ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt     360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg     420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag     480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga     540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat     600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg     660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa     720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa     780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca     840

gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc     900

cgagcaatga tctcccgctg gtactttgat gtgactgaag ggaagtgtgc cccattcttt     960

tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg    1020

tgtggcagcg ccatgtccca aagtttactc aagactaccc aggaacctct ggccgagat    1080

cctgttaaac ttcctacaac agcagccagt acccctgatg ccgttgacaa gtatctcgag    1140
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-73-

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acacctgggg atgagaatga acatgcccat ttccagaaag ccaaagagag gcttgaggcc    1200

aagcaccgag agagaatgtc ccaggtcatg agagaatggg aagaggcaga acgtcaagca    1260

aagaacttgc ctaaagctga taagaaggca gttatccagc atttccagga gaaagtggaa    1320

tctttggaac aggaagcagc caacgagaga cagcagctgg tggagacaca catggccaga    1380

gtggaagcca tgctcaatga ccgccgccgc ctggccctgg agaactacat caccgctctg    1440

caggctgttc ctcctcggcc tcgtcacgtg ttcaatatgc taaagaagta tgtccgcgca    1500

gaacagaagg acagacagca caccctaaag catttcgagc atgtgcgcat ggtggatccc    1560

aagaaagccg ctcagatccg gtcccaggtt atgacacacc tccgtgtgat ttatgagcgc    1620

atgaatcagt ctctctccct gctctacaac gtgcctgcag tggccgagga gattcaggat    1680

gaagttgatg agctgcttca gaaagagcaa aactattcag atgacgtctt ggccaacatg    1740

attagtgaac caaggatcag ttacggaaac gatgctctca tgccatcttt gaccgaaacg    1800

aaaaccaccg tggagctcct tcccgtgaat ggagagttca gcctggacga tctccagccg    1860

tggcattctt ttggggctga ctctgtgcca gccaacacag aaaacgaagt tgagcctgtt    1920

gatgcccgcc ctgctgccga ccgaggactg accactcgac caggttctgg gttgacaaat    1980

atcaagacgg aggagatctc tgaagtgaag atggatgcag aattccgaca tgactcagga    2040

tatgaagttc atcatcaaaa attggtgttc tttgcagaag atgtgggttc aaacaaaggt    2100

gcaatcattg gactcatggt gggcggtgtt gtcatagcga cagtgatcgt catcaccttg    2160

gtgatgctga agaagaaaca gtacacatcc attcatcatg gtgtggtgga ggttgacgcc    2220

gctgtcaccc cagaggagcg ccacctgtcc aagatgcagc agaacggcta cgaaaatcca    2280

acctacaagt tctttgagca gatgcagaac aagaag                              2316
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<210> 59
<211> 772
<212> PRT
<213> Homo sapiens

<400> 59

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Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1                 5                  10                 15


Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20                  25                  30


Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
                35                  40                  45


Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50                  55                  60
```

-74-

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65   70   75   80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85   90   95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
        100   105   110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
        115   120   125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
    130   135   140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145   150   155   160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165   170   175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
            180   185   190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
            195   200   205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
    210   215   220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225   230   235   240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
            245   250   255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
            260   265   270

Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
        275   280   285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
    290   295   300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305   310   315   320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

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```
Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
            580             585             590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
            595             600             605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
    610             615             620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625             630             635             640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
            645             650             655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
            660             665             670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
    675             680             685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
    690             695             700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705             710             715             720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
            725             730             735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
            740             745             750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
            755             760             765

Gln Asn Lys Lys
        770


<210>  60
<211>  2259
<212>  DNA
<213>  Homo sapiens

<400>  60
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cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga      120

ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa      180
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acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg    240

cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg    300

ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt    360

gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg    420

atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag    480

aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga    540

ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat    600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg    660

agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa    720

gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa    780

ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca    840

gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc    900

cgagcaatga tctcccgctg gtactttgat gtgactgaag ggaagtgtgc cccattcttt    960

tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg   1020

tgtggcagcg ccattcctac aacagcagcc agtacccctg atgccgttga caagtatctc   1080

gagacacctg gggatgagaa tgaacatgcc catttccaga aagccaaaga gaggcttgag   1140

gccaagcacc gagagagaat gtcccaggtc atgagagaat gggaagaggc agaacgtcaa   1200

gcaaagaact tgcctaaagc tgataagaag gcagttatcc agcatttcca ggagaaagtg   1260

gaatctttgg aacaggaagc agccaacgag agacagcagc tggtggagac acacatggcc   1320

agagtggaag ccatgctcaa tgaccgccgc cgcctggccc tggagaacta catcaccgct   1380

ctgcaggctg ttcctcctcg gcctcgtcac gtgttcaata tgctaaagaa gtatgtccgc   1440

gcagaacaga aggacagaca gcacaccta aagcatttcg agcatgtgcg catggtggat   1500

cccaagaaag ccgctcagat ccggtcccag gttatgacac acctccgtgt gatttatgag   1560

cgcatgaatc agtctctctc cctgctctac aacgtgcctg cagtggccga ggagattcag   1620

gatgaagttg atgagctgct tcagaaagag caaaactatt cagatgacgt cttggccaac   1680

atgattagtg aaccaaggat cagttacgga aacgatgctc tcatgccatc tttgaccgaa   1740

acgaaaacca ccgtggagct ccttcccgtg aatggagagt tcagcctgga cgatctccag   1800

ccgtggcatt cttttggggc tgactctgtg ccagccaaca cagaaaacga agttgagcct   1860

gttgatgccc gccctgctgc cgaccgagga ctgaccactc gaccaggttc tgggttgaca   1920

aatatcaaga cggaggagat ctctgaagtg aagatggatg cagaattccg acatgactca   1980

ggatatgaag ttcatcatca aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa   2040

ggtgcaatca ttggactcat ggtgggcggt gttgtcatag cgacagtgat cgtcatcacc   2100
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ttggtgatgc tgaagaagaa acagtacaca tccattcatc atggtgtggt ggaggttgac   2160

gccgctgtca ccccagagga gcgccacctg tccaagatgc agcagaacgg ctacgaaaat   2220

ccaacctaca agttctttga gcagatgcag aacaagaag   2259

<210> 61
<211> 753
<212> PRT
<213> Homo sapiens

<400> 61

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1   5   10   15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
                20   25   30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
            35   40   45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
        50   55   60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65   70   75   80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85   90   95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
            100   105   110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
            115   120   125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
        130   135   140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145   150   155   160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165   170   175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
            180   185   190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
        195   200   205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
    210   215   220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225   230   235   240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
            245   250   255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
            260   265   270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
        275   280   285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
    290   295   300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305   310   315   320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
            325   330   335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
        340   345   350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
        355   360   365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
    370   375   380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
385   390   395   400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
            405   410   415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
        420   425   430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
        435   440   445

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Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
    450   455   460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
465   470   475   480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
             485   490   495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
             500   505   510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
        515   520   525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
    530   535   540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
545   550   555   560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
             565   570   575

Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
        580   585   590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
        595   600   605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
    610   615   620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
625   630   635   640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
             645   650   655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
             660   665   670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
         675   680   685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
    690   695   700

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Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705   710   715   720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
                725   730   735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys
                740   745   750

Lys

<210> 62
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 62

Leu Glu Val Leu Phe Gln Gly Pro
1   5

<210> 63
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 63

Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
1   5   10

<210> 64
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 64

Ser Glu Val Lys Met Asp Ala Glu Phe Arg
1   5   10

<210> 65
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223>   Synthetic peptide

<400>   65

Arg Arg Gly Gly Val Val Ile Ala Thr Val Ile Val Gly Glu Arg
1   5   10   15

<210>   66
<211>   518
<212>   PRT
<213>   Homo sapiens

<400>   66

Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
1   5   10   15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
        20   25   30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
        35   40   45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
    50   55   60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65   70   75   80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
            85   90   95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
            100   105   110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
            115   120   125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
    130   135   140

Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
145   150   155   160

Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
            165   170   175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
            180   185   190

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```
Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
        195                 200             205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
    210             215                 220

Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
225                 230             235                 240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
            245             250                 255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
        260             265             270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
        275             280             285

Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
    290             295             300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
305             310             315                 320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
                325                 330                 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
            340             345             350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
        355             360             365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
    370             375             380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385                 390             395                 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
            405             410                 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
            420             425                 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
        435             440             445
```

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```
Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
    450             455             460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465             470             475             480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
            485             490             495

Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
        500             505             510

Val Arg His Arg Trp Lys
        515
```

<210> 67
<211> 475
<212> PRT
<213> Homo sapiens

<400> 67

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Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
1           5               10              15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
        20              25              30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
        35              40              45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
    50              55              60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65              70              75              80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
            85              90              95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
            100             105             110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
            115             120             125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
    130             135             140
```

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```
Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
145             150             155             160

Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
            165             170             175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
            180             185             190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
        195             200             205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
    210             215             220

Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
225             230             235             240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
            245             250             255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
        260             265             270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
        275             280             285

Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
    290             295             300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
305             310             315             320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
            325             330             335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
        340             345             350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
        355             360             365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
    370             375             380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385             390             395             400
```

```
Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
            405             410                 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
            420             425             430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
        435             440             445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
    450             455             460

Glu Pro Ile Leu Trp His His His His His His
465             470             475
```

<210> 68
<211> 413
<212> PRT
<213> Homo sapiens

<400> 68

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Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu
1               5               10                  15

Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu
            20              25              30

Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp
            35              40              45

Thr Gly Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile
    50              55              60

Asp Thr Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly
65              70              75              80

Phe Asp Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val
            85              90              95

Gly Glu Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu
            100             105             110

Val Asn Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly
        115             120             125

Ile Lys Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys
    130             135             140
```

Pro Ser Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala
145   150   155   160

Asn Ile Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro
                165   170   175

Val Ala Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile
            180   185   190

Glu Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu
        195   200   205

Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln
        210   215   220

Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val
225   230   235   240

Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala
                245   250   255

Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp
            260   265   270

Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr
        275   280   285

Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn
        290   295   300

Ser Ser Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln
305   310   315   320

Pro Met Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile
                325   330   335

Ser Pro Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly
            340   345   350

Phe Tyr Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala
        355   360   365

Ser Pro Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly
    370   375   380

Pro Phe Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser
385   390   395   400

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Leu Ser Glu Pro Ile Leu Trp His His His His His His
                    405   410

<210> 69
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 69

Gly Leu Ala Leu Ala Leu Glu Pro
1   5

<210> 70
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 70

Glu Val Lys Met Asp Ala Glu Phe
1   5

<210> 71
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 71

Glu Val Asn Leu Asp Ala Glu Phe
1   5

<210> 72
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 72

Leu Val Phe Phe Ala Glu Asp Val
1   5

<210> 73
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 73

Lys Leu Val Phe Phe Ala Glu Asp
1   5

<210> 74
<211> 39
<212> DNA
<213> Artificial sequence

<220>
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<400> 74
cgctttaagc ttgccaccat gggcgcactg gcccgggcg   39

<210> 75
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 75
cgctttctcg agctaatggt gatggtgatg gtgccacaaa atgggctcgc tcaaaga   57

<210> 76
<211> 4
<212> PRT
<213> Artificial sequence

<220>
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<400> 76

Asn Leu Asp Ala
1

<210> 77
<211> 5
<212> PRT
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<220>
<223> Synthetic peptide

<400> 77

Gly Arg Arg Gly Ser
1   5

<210> 78
<211> 6
<212> PRT
<213> Artificial sequence

<220>
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<400> 78

Thr Gln His Gly Ile Arg
1   5

<210> 79
<211> 6
<212> PRT
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<220>
<223> Synthetic peptide

<400> 79

Glu Thr Asp Glu Glu Pro
1   5

<210> 80
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 80

Met Cys Ala Glu Val Lys Met Asp Ala Glu Phe Lys Asp Asn Pro
1   5   10   15

<210> 81
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 81

Asp Ala Glu Phe Arg
1   5

<210> 82
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223>   Synthetic peptide

<400>   82

Ser Glu Val Asn Leu
1   5

<210>   83
<211>   4
<212>   PRT
<213>   Artificial sequence

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<223>   Xaa = Lys or Asn

<220>
<221>   misc_feature
<222>   (2)
<223>   Xaa = Met or Leu

<220>
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<222>   (3)
<223>   Xaa = Asp

<220>
<221>   misc_feature
<222>   (4)
<223>   Xaa = Asp

<400>   83

Xaa Xaa Xaa Xaa
1

FIGURE 1 (1)

ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC
M G A L A R A L L L P L L A Q W L L R A

CCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC
A P E L A P A P F T L P L R V A A A T N

CGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG
R V V A P T P G P G T P A E R H A D G L

GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG
A L A L E P A L A S P A G A A N F L A M

GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC
V D N L Q G D S G R G Y Y L E M L I G T

CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA
P P Q K L Q I L V D T G S S N F A V A G

ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC
T P H S Y I D T Y F D T E R S S T Y R S

AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA
K G F D V T V K Y T Q G S W T G F V G E

GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT
D L V T I P K G F N T S F L V N I A T I

TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT
F E S E N F F L P G I K W N G I L G L A

TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA
Y A T L A K P S S S L E T F F D S L V T

CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT
Q A N I P N V F S M Q M C G A G L P V A

GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA
G S G T N G G S L V L G G I E P S L Y K

GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA
G D I W Y T P I K E E W Y Y Q I E I L K

TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC
L E I G G Q S L N L D C R E Y N A D K A

ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG
I V D S G T T L L R L P Q K V F D A V V

GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC
E A V A R A S L I P E F S D G F W T G S

CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC
Q L A C W T N S E T P W S Y F P K I S I

TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC
Y L R D E N S S R S F R I T I L P Q L Y

ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA
I Q P M M G A G L N Y E C Y R F G I S P

TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC
S T N A L V I G A T V M E G F Y V I F D

AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA

FIGURE 1 (2)

R A Q K R V G F A A S P C A E I A G A A

GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT
V S E I S G P F S T E D V A S N C V P A

CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA
Q S L S E P I L W I V S Y A L M S V C G

GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC
A I L L V L I V L L L L P F R C Q R R P

CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA
R D P E V V N D E S S L V R H R W K

GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC
AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT
GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC
CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA
AAAA

FIGURE 2 (1)

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC
M A Q A L P W L L L W M G A G V L P A H

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG
G T Q H G I R L P L R S G L G G A P L G

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT
L R L P R E T D E E P E E P G R R G S F

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC
V E M V D N L R G K S G Q G Y Y V E M T

GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA
V G S P P Q T L N I L V D T G S S N F A

GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
V G A A P H P F L H R Y Y Q R Q L S S T

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG
Y R D L R K G V Y V P Y T Q G K W E G E

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT
L G T D L V S I P H G P N V T V R A N I

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG
A A I T E S D K F F I N G S N W E G I L

GGGCTGGCCTATGCTGAGATTGCCAGGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCT
G L A Y A E I A R L C G A G F P L N Q S

GAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATCGACCACTCGCTGTAC
E V L A S V G G S M I I G G I D H S L Y

ACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTG
T G S L W Y T P I R R E W Y Y E V I I V

CGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTACAACTATGACAAG
R V E I N G Q D L K M D C K E Y N Y D K

AGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCA
S I V D S G T T N L R L P K K V F E A A

GTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGA
V K S I K A A S S T E K F P D G F W L G

GAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCATCTCA
E Q L V C W Q A G T T P W N I F P V I S

CTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAA
L Y L M G E V T N Q S F R I T I L P Q Q

TACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATC

FIGURE 2 (2)

```
Y   L   R   P   V   E   D   V   A   T   S   Q   D   D   C   Y   K   F   A   I
TCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTC
S   Q   S   S   T   G   T   V   M   G   A   V   I   M   E   G   F   Y   V   V

TTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAG
F   D   R   A   R   K   R   I   G   F   A   V   S   A   C   H   V   H   D   E

TTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTAC
F   R   T   A   A   V   E   G   P   F   V   T   L   D   M   E   D   C   G   Y

AACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATC
N   I   P   Q   T   D   E   S   T   L   M   T   I   A   Y   V   M   A   A   I

TGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGC
C   A   L   F   M   L   P   L   C   L   M   V   C   Q   W   R   C   L   R   C

CTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCA
L   R   Q   Q   H   D   D   F   A   D   D   I   S   L   L   K

TGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTA
GGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAAATGC
CTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAG
GAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAA
TTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCT
TTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACAC
GCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTT
CCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGG
GACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGAAAAAAAAAAAAA
```

FIGURE 3 (1)

```
ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC
M  A  Q  A  L  P  W  L  L  L  W  M  G  A  G  V  L  P  A  H

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG
G  T  Q  H  G  I  R  L  P  L  R  S  G  L  G  G  A  P  L  G

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT
L  R  L  P  R  E  T  D  E  E  P  E  E  P  G  R  R  G  S  F

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC
V  E  M  V  D  N  L  R  G  K  S  G  Q  G  Y  Y  V  E  M  T

GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA
V  G  S  P  P  Q  T  L  N  I  L  V  D  T  G  S  S  N  F  A

GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
V  G  A  A  P  H  P  F  L  H  R  Y  Y  Q  R  Q  L  S  S  T

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG
Y  R  D  L  R  K  G  V  Y  V  P  Y  T  Q  G  K  W  E  G  E

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT
L  G  T  D  L  V  S  I  P  H  G  P  N  V  T  V  R  A  N  I

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG
A  A  I  T  E  S  D  K  F  F  I  N  G  S  N  W  E  G  I  L

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT
G  L  A  Y  A  E  I  A  R  P  D  D  S  L  E  P  F  F  D  S

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC
L  V  K  Q  T  H  V  P  N  L  F  S  L  Q  L  C  G  A  G  F

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC
P  L  N  Q  S  E  V  L  A  S  V  G  G  S  M  I  I  G  G  I

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT
D  H  S  L  Y  T  G  S  L  W  Y  T  P  I  R  R  E  W  Y  Y

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG
E  V  I  I  V  R  V  E  I  N  G  Q  D  L  K  M  D  C  K  E

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA
Y  N  Y  D  K  S  I  V  D  S  G  T  T  N  L  R  L  P  K  K

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT
V  F  E  A  A  V  K  S  I  K  A  A  S  S  T  E  K  F  P  D
```

FIGURE 3 (2)

```
GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT
 G   F   W   L   G   E   Q   L   V   C   W   Q   A   G   T   T   P   W   N   I
```

```
TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC
 F   P   V   I   S   L   Y   L   M   G   E   V   T   N   Q   S   F   R   I   T
```

```
ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT
 I   L   P   Q   Q   Y   L   R   P   V   E   D   V   A   T   S   Q   D   D   C
```

```
TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG
 Y   K   F   A   I   S   Q   S   S   T   G   T   V   M   G   A   V   I   M   E
```

```
GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC
 G   F   Y   V   V   F   D   R   A   R   K   R   I   G   F   A   V   S   A   C
```

```
CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG
 H   V   H   D   E   F   R   T   A   A   V   E   G   P   F   V   T   L   D   M
```

```
GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT
 E   D   C   G   Y   N   I   P   Q   T   D   E   S   T   L   M   T   I   A   Y
```

```
GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG
 V   M   A   A   I   C   A   L   F   M   L   P   L   C   L   M   V   C   Q   W
```

```
CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG
 R   C   L   R   C   L   R   Q   Q   H   D   D   F   A   D   D   I   S   L   L
```

```
AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA
 K
```

```
CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC
CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG
GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT
CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT
TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA
ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

FIGURE 4

```
ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCAG
 M  A  P  A  L  H  W  L  L  L  W  V  G  S  G  M  L  P  A  Q
GGAACCCATCTCGGCATCCGGCTGCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC
 G  T  H  L  G  I  R  L  P  L  R  S  G  L  A  G  P  P  L  G
CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT
 L  R  L  P  R  E  T  D  E  E  S  E  E  P  G  R  R  G  S  F
GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC
 V  E  M  V  D  N  L  R  G  K  S  G  Q  G  Y  Y  V  E  M  T
GTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACTTTGCA
 V  G  S  P  P  Q  T  L  N  I  L  V  D  T  G  S  S  N  F  A
GTGGGGGCTGCCCCACACCCTTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
 V  G  A  A  P  H  P  F  L  H  R  Y  Y  Q  R  Q  L  S  S  T
TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA
 Y  R  D  L  R  K  G  V  Y  V  P  Y  T  Q  G  K  W  E  G  E
CTGGGCACCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT
 L  G  T  D  L  V  S  I  P  H  G  P  N  V  T  V  R  A  N  I
GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAACTGGGAGGGCATCCTA
 A  A  I  T  E  S  D  K  F  F  I  N  G  S  N  W  E  G  I  L
GGGCTGGCCTATGCTGAGATTGCCAGGCCCGACGACTCTTTGGAGCCCTTCTTTGACTCC
 G  L  A  Y  A  E  I  A  R  P  D  D  S  L  E  P  F  F  D  S
CTGGTGAAGCAGACCCACATTCCCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC
 L  V  K  Q  T  H  I  P  N  I  F  S  L  Q  L  C  G  A  G  F
CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC
 P  L  N  Q  T  E  A  L  A  S  V  G  G  S  M  I  I  G  G  I
GACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCCGGCGGGAGTGGTATTAT
 D  H  S  L  Y  T  G  S  L  W  Y  T  P  I  R  R  E  W  Y  Y
GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG
 E  V  I  I  V  R  V  E  I  N  G  Q  D  L  K  M  D  C  K  E
TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA
 Y  N  Y  D  K  S  I  V  D  S  G  T  T  N  L  R  L  P  K  K
GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT
 V  F  E  A  A  V  K  S  I  K  A  A  S  S  T  E  K  F  P  D
GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT
 G  F  W  L  G  E  Q  L  V  C  W  Q  A  G  T  T  P  W  N  I
TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC
 F  P  V  I  S  L  Y  L  M  G  E  V  T  N  Q  S  F  R  I  T
ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT
 I  L  P  Q  Q  Y  L  R  P  V  E  D  V  A  T  S  Q  D  D  C
TACAAGTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA
 Y  K  F  A  V  S  Q  S  S  T  G  T  V  M  G  A  V  I  M  E
GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGC
 G  F  Y  V  V  F  D  R  A  R  K  R  I  G  F  A  V  S  A  C
CATGTGCACGATGAGTTCAGGACGGCGGCAGTGGAAGGTCCGTTTGTTACGGCAGACATG
 H  V  H  D  E  F  R  T  A  A  V  E  G  P  F  V  T  A  D  M
GAAGACTGTGGCTACAACATTCCCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT
 E  D  C  G  Y  N  I  P  Q  T  D  E  S  T  L  M  T  I  A  Y
GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAGTGG
 V  M  A  A  I  C  A  L  F  M  L  P  L  C  L  M  V  C  Q  W
CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC
 R  C  L  R  C  L  R  H  Q  H  D  D  F  A  D  D  I  S  L  L
AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCCTGGACCACATCTGGGTGGTTCC
 K
CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT
CACCAACCTGCCAATGCTTCTGGCGTGACAGAACAGAGAAATCAGGCAAGCTGGATTACA
GGGCTTGCACCTGTAGGACACAGGAGAGGGAAGCAAGCAGCGTTCTGGTGGCAGGAATAT
CCTTAGGCACCACAAACTTGAGTTGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACCCT
CTGCCCAGCATCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTCCTTCCAGAAGTAC
```

TGGCGTCATACTCAGGCTACCCGGCATGTGTCCCTGTGGTACCCTGGCAGAGAAAGGGCC
AATCTCATTCCCTGCTGGCCAAAGTCAGCAGAAGAAGGTGAAGTTTGCCAGTTGCTTTAG
TGATAGGGACTGCAGACTCAAGCCTACACTGGTACAAAGACTGCGTCTTGAGATAAACAA
GAA

FIGURE 5

```
  1 MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLPRETDEE  50
    || || |||||||.|.|.||| || ||||||||||| | ||||||||||||
  1 MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLPRETDEE  50

 51 PEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFA 100
    |||||||||||||||||||||||||||||||||||||||||||||||||
 51 SEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFA 100

101 VGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPH 150
    |||||||||||||||||||||||||||||||||||||||||||||||||
101 VGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPH 150

151 GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS 200
    |||||||||||||||||||||||||||||||||||||||||||||||||
151 GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS 200

201 LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW 250
    ||||||:||:||||||||||||||.| |||||||||||||||||||||||
201 LVKQTHIPNIFSLQLCGAGFPLNQTEALASVGGSMIIGGIDHSLYTGSLW 250

251 YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKK 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
251 YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKK 300

301 VFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMG 350
    |||||||||||||||||||||||||||||||||||||||||||||||||
301 VFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMG 350

351 EVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME 400
    |||||||||||||||||||||||||||||||||||:|||||||||||||
351 EVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIME 400

401 GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQT 450
    |||||||||||||||||||||||||||||||||||||| |||||||||||
401 GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQT 450

451 DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDFADDISLL 500
    ||||||||||||||||||||||||||||||||||||||||:||||||||||
451 DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRHQHDDFADDISLL 500

501 K 501
    |
501 K 501
```

FIGURE 6 (1)

ATGGCTAGCATGACTGGTGGACAGCAAATGGGTCGCGGATCCACCCAGCACGGCATCCGG
<u>M A S M T G G Q Q M G R G S</u> T Q H G I R

CTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACC
L P L R S G L G G A P L G L R L P R E T

GACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTG
D E E P E E P G R R G S F V E M V D N L

AGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACG
R G K S G Q G Y Y V E M T V G S P P Q T

CTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCC
L N I L V D T G S S N F A V G A A P H P

TTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGC
F L H R Y Y Q R Q L S S T Y R D L R K G

GTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGC
V Y V P Y T Q G K W E G E L G T D L V S

ATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGAC
I P H G P N V T V R A N I A A I T E S D

AAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATT
K F F I N G S N W E G I L G L A Y A E I

GCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTT
A R P D D S L E P F F D S L V K Q T H V

CCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTG
P N L F S L Q L C G A G F P L N Q S E V

CTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGC
L A S V G G S M I I G G I D H S L Y T G

AGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTG
S L W Y T P I R R E W Y Y E V I I V R V

GAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATT
E I N G Q D L K M D C K E Y N Y D K S I

GTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAA
V D S G T T N L R L P K K V F E A A V K

TCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAG
S I K A A S S T E K F P D G F W L G E Q

CTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTAC
L V C W Q A G T T P W N I F P V I S L Y

CTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTG
L M G E V T N Q S F R I T I L P Q Q Y L

CGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAG

FIGURE 6 (2)

```
    R  P  V  E  D  V  A  T  S  Q  D  D  C  Y  K  F  A  I  S  Q

TCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGAT
    S  S  T  G  T  V  M  G  A  V  I  M  E  G  F  Y  V  V  F  D

CGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGG
    R  A  R  K  R  I  G  F  A  V  S  A  C  H  V  H  D  E  F  R

ACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATT
    T  A  A  V  E  G  P  F  V  T  L  D  M  E  D  C  G  Y  N  I

CCACAGACAGATGAGTCATGA
    P  Q  T  D  E  S  *
```

FIGURE 7 (1)

ATGGCTAGCATGACTGGTGGACAGCAAATGGGTCGCGGATCGATGACTATCTCTGACTCT
<u>M A S M T G G Q Q M G R G S M T I S D S</u>

CCGCGTGAACAGGACGGATCCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTG
<u>P R E Q D G S</u> T Q H G I R L P L R S G L

GGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCC
G G A P L G L R L P R E T D E E P E E P

GGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGC
G R R G S F V E M V D N L R G K S G Q G

TACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACA
Y Y V E M T V G S P P Q T L N I L V D T

GGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAG
G S S N F A V G A A P H P F L H R Y Y Q

AGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGCGTGTATGTGCCCTACACCCAG
R Q L S S T Y R D L R K G V Y V P Y T Q

GGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTC
G K W E G E L G T D L V S I P H G P N V

ACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCC
T V R A N I A A I T E S D K F F I N G S

AACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTG
N W E G I L G L A Y A E I A R P D D S L

GAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAG
E P F F D S L V K Q T H V P N L F S L Q

CTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGC
L C G A G F P L N Q S E V L A S V G G S

ATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATC
M I I G G I D H S L Y T G S L W Y T P I

CGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTG
R R E W Y Y E V I I V R V E I N G Q D L

AAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAAC
K M D C K E Y N Y D K S I V D S G T T N

CTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCC
L R L P K K V F E A A V K S I K A A S S

ACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGC
T E K F P D G F W L G E Q L V C W Q A G

ACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAAC
T T P W N I F P V I S L Y L M G E V T N

FIGURE 7 (2)

```
CAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCC
 Q   S   F   R   I   T   I   L   P   Q   Q   Y   L   R   P   V   E   D   V   A
```

```
ACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATG
 T   S   Q   D   D   C   Y   K   F   A   I   S   Q   S   S   T   G   T   V   M
```

```
GGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGC
 G   A   V   I   M   E   G   F   Y   V   V   F   D   R   A   R   K   R   I   G
```

```
TTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCT
 F   A   V   S   A   C   H   V   H   D   E   F   R   T   A   A   V   E   G   P
```

```
TTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCATGA
 F   V   T   L   D   M   E   D   C   G   Y   N   I   P   Q   T   D   E   S   *
```

FIGURE 8 (1)

```
ATGACTCAGCATGGTATTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCTCCACTGGGT
 M  T  Q  H  G  I  R  L  P  L  R  S  G  L  G  G  A  P  L  G  -

CTGCGTCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT
 L  R  L  P  R  E  T  D  E  E  P  E  E  P  G  R  R  G  S  F  -

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC
 V  E  M  V  D  N  L  R  G  K  S  G  Q  G  Y  Y  V  E  M  T  -

GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA
 V  G  S  P  P  Q  T  L  N  I  L  V  D  T  G  S  S  N  F  A  -

GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
 V  G  A  A  P  H  P  F  L  H  R  Y  Y  Q  R  Q  L  S  S  T  -

TACCGGGACCTCCGGAAGGGCGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG
 Y  R  D  L  R  K  G  V  Y  V  P  Y  T  Q  G  K  W  E  G  E  -

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT
 L  G  T  D  L  V  S  I  P  H  G  P  N  V  T  V  R  A  N  I  -

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG
 A  A  I  T  E  S  D  K  F  F  I  N  G  S  N  W  E  G  I  L  -

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT
 G  L  A  Y  A  E  I  A  R  P  D  D  S  L  E  P  F  F  D  S  -

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC
 L  V  K  Q  T  H  V  P  N  L  F  S  L  Q  L  C  G  A  G  F  -

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC
 P  L  N  Q  S  E  V  L  A  S  V  G  G  S  M  I  I  G  G  I  -

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT
 D  H  S  L  Y  T  G  S  L  W  Y  T  P  I  R  R  E  W  Y  Y  -

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG
 E  V  I  I  V  R  V  E  I  N  G  Q  D  L  K  M  D  C  K  E  -

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA
 Y  N  Y  D  K  S  I  V  D  S  G  T  T  N  L  R  L  P  K  K  -

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT
 V  F  E  A  A  V  K  S  I  K  A  A  S  S  T  E  K  F  P  D  -

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT
 G  F  W  L  G  E  Q  L  V  C  W  Q  A  G  T  T  P  W  N  I  -

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTTCGCATCACC
 F  P  V  I  S  L  Y  L  M  G  E  V  T  N  Q  S  F  R  I  T  -

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT
 I  L  P  Q  Q  Y  L  R  P  V  E  D  V  A  T  S  Q  D  D  C  -
```

FIGURE 8 (2)

```
TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG
 Y  K  F  A  I  S  Q  S  S  T  G  T  V  M  G  A  V  I  M  E   -

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC
 G  F  Y  V  V  F  D  R  A  R  K  R  I  G  F  A  V  S  A  C   -
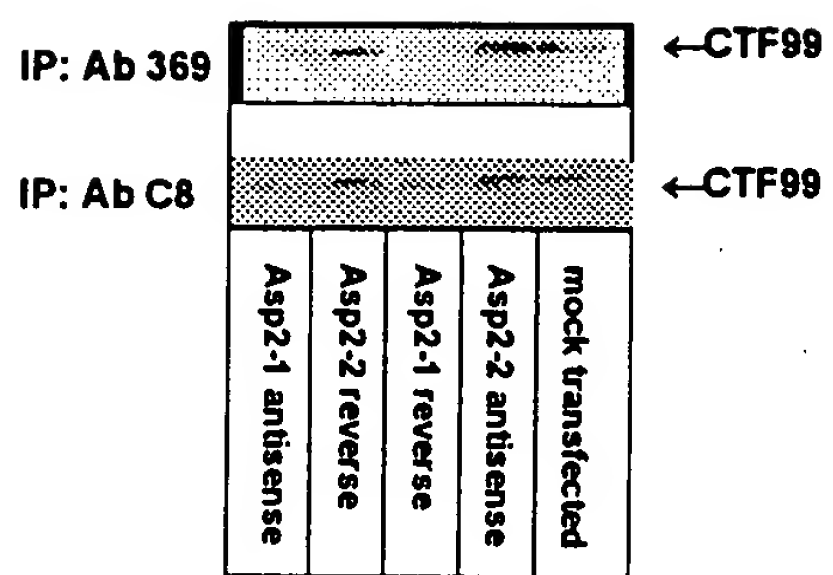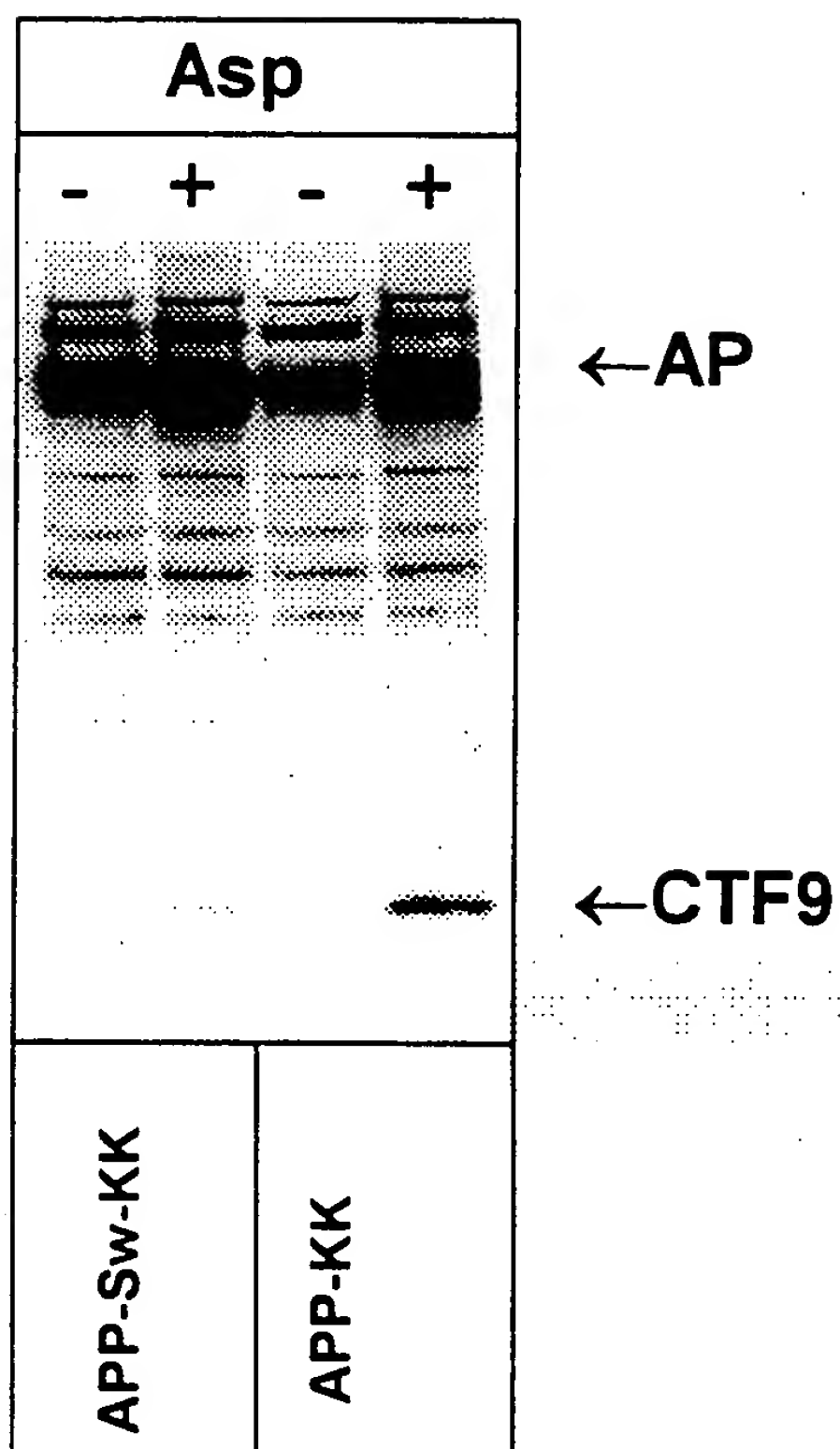
CATTAG
 H  *
```

FIGURE 9

FIGURE 10

FIGURE 11

MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLPRETDEE
PEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFA
VGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPH
GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKK
VFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMG
EVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQT
DES

FIGURE 12

MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLPRETDEE
PEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFA
VGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPH
GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKK
VFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMG
EVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQT
DESHHHHHH